In the Claims

1-120. (canceled)

121. (currently amended) A method of genotyping comprising determining the identity of a nucleotide at a ~~PCTA-1 related~~ biallelic marker of SEQ ID NO: 12, or the complement of said nucleotide, in a biological sample, wherein said biallelic marker is selected from the group consisting of biallelic markers of SEQ ID No:1 located at positions 402 (A2), 67092 (A30), 68525 (A41), 82234 (A55), 82393 (A57), and 87713 (A75).

122. (currently amended) ~~A~~ The method according to claim 121, wherein said biological sample is derived from a single subject.

123. (currently amended) ~~A~~ The method according to claim 122, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said individual's genome.

124. (currently amended) ~~A~~ The method according to claim 121, wherein said biological sample is derived from multiple subjects.

125. (currently amended) ~~A~~ The method according to claim 121, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.

126. (currently amended) ~~A~~ The method according to claim 125, wherein said amplifying is performed by PCR.

127. (currently amended) ~~A~~ The method according to claim 121, wherein said determining is performed by a hybridization assay.

128. (currently amended) ~~A~~ The method according to claim 121, wherein said determining is performed by a sequencing assay.

129. (currently amended) ~~A~~ The method according to claim 121, wherein said determining is performed by a microsequencing assay.

130. (currently amended) ~~A~~ The method according to claim 121, wherein said determining is performed by an enzyme-based mismatch detection assay.

131. (currently amended) A method of estimating the frequency of an allele of a ~~PCTA-1-related~~ biallelic marker of SEQ ID NO: 12 in a population comprising:

a) genotyping individuals from said population for said biallelic marker according to the method of claim 121; and

b) determining the proportional representation of said biallelic marker in said population.

132. (currently amended) A method of detecting an association between a genotype and a trait, comprising the steps of:

a) performing the method of claim 131 to determine the frequency of at least one biallelic marker of SEQ ID NO: 12 in trait positive population;

b) performing the method of claim 131 to determine the frequency of at least one biallelic marker of SEQ ID NO: 12 in a control population; and

c) determining whether a statistically significant association exists between said genotype and said trait, wherein said trait is familial or sporadic prostate cancer.

~~A method of detecting an association between a genotype and a trait, comprising the steps of:~~

~~a) determining the frequency of at least one PCTA-1-related biallelic marker in trait positive population according to the method of claim 131;~~

~~b) determining the frequency of at least one PCTA-1-related biallelic marker in a control population according to the method of claim 131; and~~

~~c) determining whether a statistically significant association exists between said genotype and said trait.~~

133. (currently amended) A method of estimating the frequency of a haplotype for a set of biallelic markers of SEQ ID NO: 12 in a population, comprising:

a) genotyping at least one ~~PCTA-1-related~~ biallelic marker of SEQ ID NO: 12 according to claim 122 for each individual in said population;

b) genotyping a second biallelic marker of SEQ ID NO: 12 by determining the identity of the ~~nucleotides~~ nucleotide at said second biallelic marker for both copies of said second biallelic marker present in the genome of each individual in said population; and

c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

134. (currently amended) ~~A~~ The method according to claim 133, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark algorithm, or an expectation-maximization algorithm.

135. (currently amended) A method of detecting an association between a haplotype and a trait, comprising the steps of:

a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 133;

b) estimating the frequency of said haplotype in a control population according to the method of claim 133; and

c) determining whether a statistically significant association exists between said haplotype and said trait, wherein said trait is familial or sporadic prostate cancer.

136. (currently amended) ~~A~~ The method according to claim 132, wherein said genotyping steps a) and b) are performed on a single pooled biological sample derived from each of said populations.

137. (currently amended) ~~A~~ The method according to claim 132, wherein said genotyping steps a) and b) performed separately on biological samples derived from each individual in said populations.

138-139. (canceled)

140. (previously added) The method according to claim 132, wherein said control population is a trait negative population.

141. (previously amended) The method according to claim 132, wherein said control population is a random population.

142-149. (canceled)

150. (currently amended) A method of determining whether an individual is at risk of developing familial or sporadic prostate cancer, comprising:

a) genotyping at least one ~~PCTA-1-related~~ biallelic marker of SEQ ID NO: 12 according to the method of claim 123; ~~and~~

b) determining if the individual has a biallelic marker or combination of biallelic markers that is associated with familial or sporadic prostate cancer; and

c~~b~~) correlating the result of step b) ~~a)~~ with a biallelic marker or one or more combinations of biallelic markers that are~~is~~ associated with a risk of developing familial or sporadic prostate cancer;

wherein:

for familial cases of prostate cancer said biallelic marker or combinations of biallelic markers are selected from the group consisting of: 1) A30 and A41; 2) A30 and A57; 3); A30 and A55; 4) A2 and A41; 5) A2 and A30; 6) A30 and A75; 7) A2 and A55; 8) A2, A30, and A41; 9) A2, A30, and A57; 10) A2, A30, and A55; 11) A30, A41, and A55; 12) A30, A57, and A75; 13) A30, A55, and A75; 14) A30, A41, and A75; 15) A30, A55, and A57; 16) A30, A41, and A57; 17) A2, A30, A55, and A57; 18) A2, A30, A57, and A75; 19) A2, A30, A55, and A75; 20) A2, A30, A41, and A57; 21) A2, A30, A41, and A55; 22) A2, A30, A41, and A75; 23) A30, A55, A57, and A75; 24) A30, A41, A55, and A75; 25) A30, A41, A55, and A57; 26) A30, A41, A57, and A75 and A30; and 27) A30; and

for sporadic cases of prostate cancer said combinations of biallelic markers are selected from the group consisting of: 1) A2 and A55; 2) A2 and A57; 3) A41 and A55; 4) A41 and A57; 5) A2 and A41; 6) A30 and A75; 7) A2, A41, and A55; 8) A2, A55, and A57; 9) A2, A41, and A57; 10) A41, A55, and A57; 11) A2, A55, and A75; 12) A30, A41, and A57; 13) A30, A41, and A55; 14) A2, A30, A41, and A57; 15) A2, A30, A41, and A55; 16) A2, A41, A55, and A57; 17) A2, A41, A55, and A75; and 18) A30, A41, A55, and A57.

151-164. (canceled)

165. (previously added) The method according to claim 135, wherein said control population is a trait negative population.

166. (previously added) The method according to claim 135, wherein said control population is a random population.

167-182. (canceled)